



# SEQUENCE LISTING

<110> VisiGen Biotechnologies, Inc.

<120> REAL-TIME SEQUENCE DETERMINATION

<130> 00007/01PCT

<140> PCT/US01/21811

<141> 2001-07-09

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<151> 2000-07-07

<160> 57

<170> PatentIn version 3.1

<210> 1

<211> 19

<212> DNA

<213> Artificial

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<223> Primer strand used to test incorporation of gamma-tagged  
dNTPs using Taq DNA Polymerase I.

<220>

<221> Primer

<222> (1)..(19)

<223> 5 ' to 3' primer strand called TOP

<400> 1  
ggtactaagc ggccgcatg  
19

<210> 2

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<213> Artificial

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<223> Templates strand used to test incorporation of  
gamma-tagged dNTPs  
using Taq DNA Polymerase I.

<220>

<221> Template  
<222> (1)..(21)  
<223> 3' to 5' template strand BOT-T

<400> 2  
ccatgattcg ccggcgtact c  
21

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dNTPs  
using Taq DNA Polymerase I.

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<222> (1)..(21)  
<223> 3' to 5' template strand called BOT-C

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ccatgattcg ccggcgtacc c  
21

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dNTPs  
using Taq DNA Polymerase I.

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ccatgattcg ccggcgtacg c  
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dNTPs  
using Taq DNA Polymerase I.

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dNTPs  
using Taq DNA Polymerase I.

<220>  
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<223> 3' to 5' template strand called BOT-3T

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ccatgattcg ccggcggtact ttc  
23

<210> 7  
<211> 23  
<212> DNA  
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dNTPs

using Taq DNA Polymerase I.

<220>

<221> Template

<222> (1)..(23)

<223> 3' to 5' template strand called BOT-Sau

<400> 7

ccatgattcg ccggcgtacc tag

23

<210> 8

<211> 38

<212> DNA

<213> Thermus aquaticus

<220>

<221> primer\_bind

<222> (1)..(38)

<223> TAQ forward primer

<400> 8

gcgaattcat gagggggatg ctgcccctct ttgagccc

38

<210> 9

<211> 37

<212> DNA

<213> Thermus aquaticus

<220>

<221> primer\_bind

<222> (1)..(37)

<223> TAQ Pol I Reverse Primer

<400> 9

gcgaattcac cctccttggc ggagcgccag tcctccc

37

<210> 10

<211> 37

<212> DNA

<213> Thermus aquaticus

<220>

<221> misc\_feature

<222> (1)..(37)

<223> Taq Pol I A293 Trunk

<400> 10

aatccatggg ccctggagga ggccccctgg cccccgc  
37

<210> 11

<211> 832

<212> PRT

<213> Thermus aquaticus

<400> 11

Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu  
1 5 10 15

Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly  
20 25 30

Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala  
35 40 45

Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val  
50 55 60

Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly  
65 70 75 80

Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu  
85 90 95

Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu  
100 105 110

Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys  
115 120 125

Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp  
130 135 140

Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly  
145 150 155 160

Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro  
165 170 175

Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn  
180 185 190

Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu  
195 200 205

Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu  
210 215 220

Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys  
225 230 235 240

Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val  
245 250 255

Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe  
260 265 270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
275 280 285

Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
290 295 300

Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp  
305 310 315 320

Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro  
325 330 335

Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu  
340 345 350

Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro  
355 360 365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
370 375 380

Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
385 390 395 400

Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu  
405 410 415

Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu  
420 425 430

Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly  
435 440 445

Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala  
450 455 460

Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His  
465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
485 490 495

Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg  
500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
515 520 525

Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr

530

535

540

Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu  
 545 550 555 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 580 585 590

Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala  
 595 600 605

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 610 615 620

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr  
 625 630 635 640

Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro  
 645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
 660 665 670

Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
 675 680 685

Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
 690 695 700

Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val  
 705 710 715 720

Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg  
 725 730 735



Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
740 745 750

Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
755 760 765

Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His  
770 775 780

Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala  
785 790 795 800

Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro  
805 810 815

Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu  
820 825 830

<210> 12

<211> 19

<212> PRT

<213> Thermus aquaticus

<220>

<221> MISC\_FEATURE

<222> (2)..(4)

<223> Residues in native protein are Ser Trp Met

<220>

<221> MISC\_FEATURE

<222> (6)..(6)

<223> Residue in native protein is Gly

<220>

<221> MISC\_FEATURE

<222> (8)..(9)

<223> Residues in native protein are Pro Arg

<400> 12

Ala Xaa Xaa Xaa Phe Xaa Val Xaa Xaa Glu Ala Val Asp Pro Leu Met

1

5

10

15

Arg Arg Ala

<210> 13

<211> 32

<212> DNA

<213> *Thermus aquaticus*

<220>

<221> mutation

<222> (14)..(15)

<223> Residue 643 Ala to Cys mutation forward primer: Codon GCC mutated to TGC

<400> 13

ccacacggag acctgcagct ggatgttcgg cg

32

<210> 14

<211> 32

<212> DNA

<213> *Thermus aquaticus*

<220>

<221> mutation

<222> (18)..(18)

<223> Residue 643 Ala to Cys mutation reverse primer: antisense  
Codon GGC mutated to  
GCA

<400> 14

cgccgaacat ccacgagcag gtctccgtgt gg

32

<210> 15

<211> 35

<212> DNA

<213> *Thermus aquaticus*

<220>

<221> mutation

<222> (16)..(16)

<223> Residue 647 Phe to Cys mutation forward primer: Codon ttc mutated to tgc

<400> 15  
ccgccagctg gatgtgcggc gtcccccgagg aggcc  
35

<210> 16  
<211> 35  
<212> DNA  
<213> *Thermus aquaticus*

<220>  
<221> mutation  
<222> (20)..(20)  
<223> Residue 647 Phe to Cys mutation reverse primer: antisense  
Codon gAa mutated to  
gCa

<400> 16  
ggcctcccgagg gggacgccgc acatccacgt ggcgg  
35

<210> 17  
<211> 37  
<212> DNA  
<213> *Thermus aquaticus*

<220>  
<221> mutation  
<222> (19)..(20)  
<223> Residue 649 Val to Cys mutation forward primer: Codon  
gtc mutated to tgc

<400> 17  
gccagctgga tgttcggctg cccccgggagg gccgtgg  
37

<210> 18  
<211> 37  
<212> DNA  
<213> *Thermus aquaticus*

<220>

<221> mutation  
<222> (18)..(19)  
<223> Residue 649 Val to Cys mutation reverse primer: antisense  
Codon gAC mutated to  
gCA

<400> 18  
ccacggcctc ccgggggcag ccgaacatcc agctggc  
37

<210> 19  
<211> 36  
<212> DNA  
<213> *Thermus aquaticus*

<220>  
<221> mutation  
<222> (13)..(15)  
<223> Residue 652 Glu to Cys mutation forward primer: Codon  
gag mutated to tgc

<400> 19  
ggcgtccccc ggtgcgccgt ggaccccctg atgcgc  
36

<210> 20  
<211> 36  
<212> DNA  
<213> *Thermus aquaticus*

<220>  
<221> mutation  
<222> (22)..(24)  
<223> Residue 652 Glu to Cys mutation reverse primer: antisense  
Codon CTC mutated to  
GCA

<400> 20  
gcgcatcagg ggtccacgg cgcaccgggg gacgcc  
36

<210> 21  
<211> 36  
<212> DNA

<213> Thermus aquaticus

<220>

<221> mutation

<222> (16)..(17)

<223> Residue 653 Ala to Cys mutation forward primer: Codon  
gcc mutated to tgc

<400> 21

ggcgtccccc gggagtgcgt ggaccccctg atgcgc  
36

<210> 22

<211> 36

<212> DNA

<213> Thermus aquaticus

<220>

<221> mutation

<222> (20)..(21)

<223> Residue 653 Ala to Cys mutation reverse primer: antisense  
Codon gGC mutated to  
gCA

<400> 22

gcgcatcagg ggggccacgc actcccgggg gacgcc  
36

<210> 23

<211> 33

<212> DNA

<213> Thermus aquaticus

<220>

<221> mutation

<222> (16)..(18)

<223> Residue 654 Val to Cys mutation forward primer: Codon  
gtg mutated to tgt

<400> 23

gtcccccgagg aggcctgtga cccctgatg cgc  
33

<210> 24

<211> 33  
<212> DNA  
<213> Thermus aquaticus  
  
<220>  
<221> mutation  
<222> (16)..(18)  
<223> Residue 654 Val to Cys mutation reverse primer: antisense  
Codon CAC mutated to  
ACA

<400> 24  
gcgcatcagg gggtcacagg cctcccgggg gac  
33

<210> 25  
<211> 33  
<212> DNA  
<213> Thermus aquaticus

<220>  
<221> mutation  
<222> (16)..(17)  
<223> Residue 655 Asp to Cys mutation forward primer: Codon  
gac mutated to tgc

<400> 25  
ccccgggagg ccgtgtgccc cctgatgcgc cgg  
33

<210> 26  
<211> 33  
<212> DNA  
<213> Thermus aquaticus

<220>  
<221> mutation  
<222> (17)..(18)  
<223> Residue 655 Asp to Cys mutation reverse primer: antisense  
Codon gTC mutated to  
gCA

<400> 26  
ccggcgcac agggggcaca cggcctccc ggg  
33

<210> 27  
<211> 33  
<212> DNA  
<213> *Thermus aquaticus*  
  
<220>  
<221> mutation  
<222> (16)..(17)  
<223> Residue 656 Pro to Cys mutation reverse primer: Codon  
ccc mutated to tgc

<400> 27  
cgggaggccg tggactgcct gatgcgccgg gcg  
33

<210> 28  
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<212> DNA  
<213> *Thermus aquaticus*  
  
<220>  
<221> mutation  
<222> (17)..(18)  
<223> Residue 656 Pro to Cys mutation reverse primer: antisense  
Codon gGG mutated to  
gCA

<400> 28  
cgccccggcgc atcaggcagt ccacggcctc ccg  
33

<210> 29  
<211> 30  
<212> DNA  
<213> *Thermus aquaticus*

<220>  
<221> mutation  
<222> (13)..(15)  
<223> Residue 657 Leu to Cys mutation forward primer: Codon  
ctg mutated to tgc

<400> 29  
gccgtggacc cctgcatgcg ccgggcggcc

30

<210> 30  
<211> 30  
<212> DNA  
<213> *Thermus aquaticus*  
  
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<222> (16)..(18)  
<223> Residue 657 Leu to Cys mutation reverse primer: antisense  
Codon CAG mutated to  
GCA

<400> 30  
ggccgcccgg cgcatgcagg ggtccacggc  
30

<210> 31  
<211> 30  
<212> DNA  
<213> *Thermus aquaticus*

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<221> mutation  
<222> (16)..(18)  
<223> Residue 658 Met to Cys mutation forward primer: Codon  
atg mutated to tgc

<400> 31  
gccgtggacc ccctgtgtcg ccgggcggcc  
30

<210> 32  
<211> 30  
<212> DNA  
<213> *Thermus aquaticus*

<220>  
<221> mutation  
<222> (13)..(15)  
<223> Residue 658 Met to Cys mutation reverse primer: antisense  
Codon CAT mutated to  
ACA



<400> 32  
ggccgcccgg cgacacaggg ggtccacggc  
30

<210> 33  
<211> 36  
<212> DNA  
<213> Thermus aquaticus

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<221> mutation  
<222> (19)..(19)  
<223> Residue 659 Arg to Cys mutation forward primer: Codon  
cgc mutated to tgc

<400> 33  
gccgtggacc ccctgatgtg ccgggaggcc aagacc  
36

<210> 34  
<211> 36  
<212> DNA  
<213> Thermus aquaticus

<220>  
<221> mutation  
<222> (18)..(18)  
<223> Residue 659 Arg to Cys mutation reverse primer: antisense  
Codon gcG mutated to  
gcA

<400> 34  
ggtcttggcc gcccggcaca tcagggggtc cacggc  
36

<210> 35  
<211> 33  
<212> DNA  
<213> Thermus aquaticus

<220>  
<221> mutation  
<222> (16)..(18)  
<223> Residue 660 Arg to Cys mutation forward primer: Codon  
cgg mutated to tgc

<400> 35  
gacccccctga tgcgctgcgc ggccaagacc atc  
33

<210> 36  
<211> 33  
<212> DNA  
<213> *Thermus aquaticus*

<220>  
<221> mutation  
<222> (16)..(18)  
<223> Residue 660 Arg to Cys mutation reverse primer: antisense  
Codon CcG mutated to  
GcA

<400> 36  
gatgggtcttg gccgcgcagc gcatcagggg gtc  
33

<210> 37  
<211> 33  
<212> DNA  
<213> *Thermus aquaticus*

<220>  
<221> mutation  
<222> (16)..(18)  
<223> Residue 661 Ala to Cys mutation forward primer: Codon  
gcg mutated to tgc

<400> 37  
cccctgatgc gccggtgcgc caagaccatc aac  
33

<210> 38  
<211> 33  
<212> DNA  
<213> *Thermus aquaticus*

<220>  
<221> mutation  
<222> (16)..(18)  
<223> Residue 661 Ala to Cys mutation reverse primer: antisense

Codon CGC mutated to  
GCA

<400> 38  
gttgatggtc ttggcgcacc ggcgcatcag ggg  
33

<210> 39  
<211> 19  
<212> PRT  
<213> Thermus aquaticus

<220>  
<221> variant  
<222> (1)..(1)  
<223> Taq Pol I Residues 643 to 661; Residue 643 ala to cys  
variant

<400> 39

Cys	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro	Leu	Met
1				5					10					15	

Arg Arg Ala

<210> 40  
<211> 19  
<212> PRT  
<213> Thermus aquaticus

<220>  
<221> variant  
<222> (5)..(5)  
<223> Taq Pol I Residues 643 to 661; Residue 647 phe to cys  
variant

<400> 40

Ala	Ser	Trp	Met	Cys	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro	Leu	Met
1				5					10					15	

Arg Arg Ala

<210> 41  
<211> 19  
<212> PRT  
<213> Thermus aquaticus

<220>  
<221> variant  
<222> (7)..(7)  
<223> Taq Pol I Residues 643 to 661; Residue 649 val to cys  
variant

<400> 41

Ala	Ser	Trp	Met	Phe	Gly	Cys	Pro	Arg	Glu	Ala	Val	Asp	Pro	Leu	Met
1				5					10					15	

Arg Arg Ala

<210> 42  
<211> 19  
<212> PRT  
<213> Thermus aquaticus

<220>  
<221> variant  
<222> (10)..(10)  
<223> Taq Pol I Residues 643 to 661; Residue 652 glu to cys  
variant

<400> 42

Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Cys	Ala	Val	Asp	Pro	Leu	Met
1				5					10					15	

Arg Arg Ala

<210> 43  
<211> 19  
<212> PRT

<213> Thermus aquaticus

<220>

<221> variant

<222> (11)..(11)

<223> Taq Pol I Residues 643 to 661; Residue 653 ala to cys  
variant

<400> 43

Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Cys	Val	Asp	Pro	Leu	Met
1				5					10					15	

Arg Arg Ala

<210> 44

<211> 19

<212> PRT

<213> Thermus aquaticus

<220>

<221> variant

<222> (12)..(12)

<223> Taq Pol I Residues 643 to 661; Residue 654 val to cys  
variant

<400> 44

Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Cys	Asp	Pro	Leu	Met
1				5					10					15	

Arg Arg Ala

<210> 45

<211> 19

<212> PRT

<213> Thermus aquaticus

<220>

<221> variant

<222> (13)..(13)

<223> Taq Pol I Residues 643 to 661; Residue 655 asp to cys

variant

<400> 45

Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Cys	Pro	Leu	Met
1				5					10					15	

Arg Arg Ala

<210> 46

<211> 19

<212> PRT

<213> *Thermus aquaticus*

<220>

<221> variant

<222> (14)..(14)

<223> Taq Pol I Residues 643 to 661; Residue 656 pro to cys  
variant

<400> 46

Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Cys	Leu	Met
1				5					10					15	

Arg Arg Ala

<210> 47

<211> 19

<212> PRT

<213> *Thermus aquaticus*

<220>

<221> variant

<222> (15)..(15)

<223> Taq Pol I Residues 643 to 661; Residue 657 leu to cys  
variant

<400> 47

Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Cys Met

1 5 10 15

Arg Arg Ala

<210> 48  
<211> 19  
<212> PRT  
<213> Thermus aquaticus  
  
<220>  
<221> variant  
<222> (16)..(16)  
<223> Taq Pol I Residues 643 to 661; Residue 658 met to cys  
variant

<400> 48

Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Cys  
1 5 10 15

Arg Arg Ala

<210> 49  
<211> 19  
<212> PRT  
<213> Thermus aquaticus  
  
<220>  
<221> variant  
<222> (17)..(17)  
<223> Taq Pol I Residues 643 to 661; Residue 659 arg to cys  
variant

<400> 49

Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met  
1 5 10 15

Cys Arg Ala

<210> 50  
<211> 19  
<212> PRT  
<213> Thermus aquaticus

<220>  
<221> variant  
<222> (18)..(18)  
<223> Taq Pol I Residues 643 to 661; Residue 660 arg to cys  
variant

<400> 50

Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro	Leu	Met
1				5					10					15	

Arg Cys Ala

<210> 51  
<211> 19  
<212> PRT  
<213> Thermus aquaticus

<220>  
<221> variant  
<222> (19)..(19)  
<223> Taq Pol I Residues 643 to 661; Residue 661 ala to cys  
variant

<400> 51

Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro	Leu	Met
1				5					10					15	

Arg Arg Cys

<210> 52  
<211> 6  
<212> PRT  
<213> Thermus aquaticus

<220>



<221> variant  
<222> (1)..(1)  
<223> Taq Pol I Residues 513 to 518; Residue 513 ser to cys  
variant

<400> 52

Cys Thr Ser Ala Ala Val  
1 5

<210> 53  
<211> 6  
<212> PRT  
<213> Thermus aquaticus

<220>  
<221> variant  
<222> (2)..(2)  
<223> Taq Pol I Residues 513 to 518; Residue 514 thr to cys  
variant

<400> 53

Ser Cys Ser Ala Ala Val  
1 5

<210> 54  
<211> 6  
<212> PRT  
<213> Thermus aquaticus

<220>  
<221> variant  
<222> (3)..(3)  
<223> Taq Pol I Residues 513 to 518; Residue 515 ser to cys  
variant

<400> 54

Ser Thr Cys Ala Ala Val  
1 5

<210> 55  
<211> 6

<212> PRT  
<213> Thermus aquaticus  
  
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variant

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Ser Thr Ser Cys Ala Val  
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variant

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Ser Thr Ser Ala Cys Val  
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variant

<400> 57

Ser Thr Ser Ala Ala Cys  
1 5